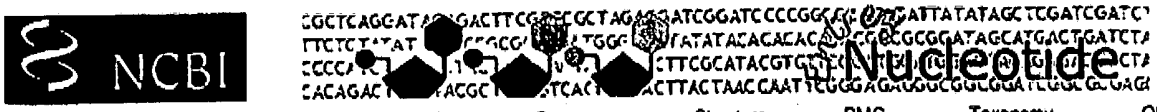

1: Z70522. C.melo mRNA (clon...[gi:1843441]

Links

```
LOCUS       CMPMEL7                  686 bp    mRNA    linear   PLN 22-JUN-2001
DEFINITION  C.melo mRNA (clone pMel7).
ACCESSION   Z70522
VERSION     Z70522.1  GI:1843441
KEYWORDS    AE1 gene.
SOURCE      Cucumis melo (muskmelon)
  ORGANISM  Cucumis melo
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE   1  (bases 1 to 686)
  AUTHORS   Aggelis,A., John,I., Karvouni,Z. and Grierson,D.
  TITLE     Characterization of two cDNA clones for mRNAs expressed during
            ripening of melon (Cucumis melo L.) fruits
  JOURNAL   Plant Mol. Biol. 33 (2), 313-322 (1997)
  MEDLINE   97188564
   PUBMED   9037149
REFERENCE   2  (bases 1 to 686)
  AUTHORS   Aggelis,A., John,I., Karvouni,Z. and Grierson,D.
  TITLE     Characterization of two cDNA clones for mRNAs expressed during
            ripening of Melon (Cucumis melo L.) fruits
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 686)
  AUTHORS   John,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-1996) John I., The University of Nottingham,
            Physiology and Environmental Science, Sutton Bonington Campus,
            Loughborough, United kingdom, LE12 5RD
FEATURES             Location/Qualifiers
     source          1..686
                     /organism="Cucumis melo"
                     /mol_type="mRNA"
                     /cultivar="Cantaloupe charentais"
                     /db_xref="taxon:3656"
                     /clone="pMEL7"
                     /cell_type="pericarp"
                     /tissue_type="fruit"
                     /clone_lib="lambda UNI-ZAP"
                     /dev_stage="ripe fruit"
     mRNA            <1..686
     5'UTR           1..30
     CDS             31..486
                     /codon_start=1
                     /product="unknown"
                     /protein_id="CAA94433.1"
                     /db_xref="GI:1843442"
                     /db_xref="SPTREMBL:P93095"
```

```
                     /translation="MSLIGKLVSELEINAAAEKFYEIFKDQCFQVPNITPRCIQQVEI
                     HGTNWDGHGHGSIKSWYYTIDGKAEVFKERVEFHDDKLLIVLDGVGGDVFKNYKSFKP
                     AYQFVPKDRNHCQAILSIEYEKLHHGSPDPHKYIDLMIGITNDIGSHIK"
     3'UTR           487..686
     polyA_signal    646..651
     polyA_site      686
BASE COUNT      211 a     97 c    135 g    243 t
ORIGIN
        1 tctatatcta gagatagaag gtttaaaatc atgtctctaa ttggaaagct tgtgagtgaa
       61 ttagagatca atgcagctgc tgagaaattt tacgaaatat tcaaagatca atgttttcag
      121 gttcccaata taacccccag atgcattcaa caagttgaaa ttcatggtac taattgggat
      181 ggccatggac atggctctat caagtcttgg tattacacta ttgatggcaa ggcagaagtt
      241 tttaaggaac gggtcgagtt tcacgatgat aaattgttga tagtcttgga tggagtggga
      301 ggagatgtgt tcaaaaatta taaaagcttt aaaccagctt accaatttgt acctaaggat
      361 cgtaaccatt gccaggcaat tctgagtata gagtatgaga aacttcatca tgggtctcct
      421 gatcctcata agtatattga cctcatgatt ggtatcacta acgacattgg atctcacatt
      481 aaataagtat ttaatgtctg tcacattctc aagtgtggct tgttaatttg ttgtgggaaa
      541 gttatatttt attttgaagt aattttcgtg tggttgatta tgtatctttg ctattttgct
      601 tttatatttc aataagttat atggtttata taatattaca aagtaaataa aatccaagga
      661 tcatcccttg tttatgtttc gttatt
//
```

EXHIBIT D

1: Nucleic Acids Res. 1991 Apr 11;19(7):1571-6. Related Articles, Linl

Upstream sequences of rice proliferating cell nuclear antigen (PCNA) gene mediate expression of PCNA-GUS chimeric gene i meristems of transgenic tobacco plants.

Kosugi S, Suzuka I, Ohashi Y, Murakami T, Arai Y.

Institute of Applied Biochemistry, University of Tsukuba, Ibaraki, Japan.

The transgenic tobacco plants have been generated that express the E. coli beta-glucuronidase (GUS) gene under control of the promoter from the rice proliferating cell nuclear antigen (PCNA, DNA polymerase auxiliary protein gene. GUS expression detected in situ by staining with the chromogenic substrate, 5-bromo-4-chloro-3-indolyl-beta-D-glucuronide (X-Gluc), was restricted to meristems in the organs of the transgenic tobacco plants. This expression responded to the phytohormones which promote callus formation. Furthermore, in situ thymidine uptake showed that the GUS expression pattern corresponded well to the active sites of DNA synthesis. Deletion analysis of the 5' upstream sequence confined the GUS expression pattern to fragment extending 263 bp upstream of the transcription start site of the rice PCNA gene. Thus, we have identified this fragment as a main regulatory element of the rice PCNA gene promoter.

PMID: 1709277 [PubMed - indexed for MEDLINE]

EXHIBIT E

1: Plant Physiol. 1994 May;105(1):357-67. Related Articles, Link

Identification of a light-responsive region of the nuclear gene encoding the B subunit of chloroplast glyceraldehyde 3-phosphate dehydrogenase from Arabidopsis thaliana.

Kwon HB, Park SC, Peng HP, Goodman HM, Dewdney J, Shih MC.

Department of Biological Sciences, University of Iowa, Iowa City 52242.

We report here the identification of a cis-acting region involved in light regulation of the nuclear gene (GapB) encoding the B subunit of chloroplast glyceraldehyde 3-phosphate dehydrogenase from Arabidopsis thaliana. Our results show that a 664-bp GapB promoter fragment is sufficient to confer light induction and organ-specific expression of the Escherichia coli beta-glucuronidase reporter gene (Gus) in transgenic tobacco (Nicotiana tabacum) plants. Deletion analysis indicates that the -261 to -173 upstream region of th GapB gene is essential for light induction. This region contains four direct repeats with the consensus sequence 5'-ATGAA(A/G)A-3' (Gap boxes). Deletion of all four repeats abolishes light induction completely. In addition, we have linked a 109-bp (-263 to -152) GapB upstream fragment containing the four direct repeats in two orientations to the -92 to +6 upstream sequence of the cauliflower mosaic virus 35S basal promoter. The resulting chimeric promoters are able to confer light induction and to enhance leaf-specific expression of the Gus reporter gene in transgenic tobacco plants. Based on these results we conclude that Gap boxes are essential for light regulation an organ-specific expression of the GapB gene in A. thaliana. Using gel mobilit shift assays we have also identified a nuclear factor from tobacco that interacts with GapA and GapB DNA fragments containing these Gap boxes. Competition assays indicate that Gap boxes are the binding sites for this factor. Although this binding activity is present in nuclear extracts from leaves and roots of light-grown or dark-treated tobacco plants, the activity is less abundant in nuclear extracts prepared from leaves of dark-treated plants or from roots of greenhouse-grown plants. In addition, our data show that thi binding factor is distinct from the GT-1 factor, which binds to Box II and Bo III within the light-responsive element of the RbcS-3A gene of pea.

PMID: 8029358 [PubMed - indexed for MEDLINE]

Entrez PubMed
Overview
Help | FAQ
Tutorial
New/Noteworthy
E-Utilities

PubMed Services
Journals Database
MeSH Database
Single Citation Matcher
Batch Citation Matcher
Clinical Queries
LinkOut
Cubby

Related Resources
Order Documents
NLM Gateway
TOXNET
Consumer Health
Clinical Alerts
ClinicalTrials.gov
PubMed Central